

Luncheon Seminar at the 55th Annual Meeting of Biophysical Society of Japan

September 21 (Thu), 11:45 ~ 12:35, Room E305 (Site I)

1. Recent activities of PDBj and wwPDB

PDBj と wwPDB の最近の活動について

Genji Kurisu, Institute for Protein Research, Osaka University

The PDBj (PDB Japan, <https://pd bj.org/>) is the representative archive of macromolecular structural data by X-ray crystallography, NMR and cryo-EM, processing the deposited data from researchers in Asian and Middle-east regions, as one of the four members of the wwPDB (worldwide PDB, <https://wwpdb.org/>). In order to promote the recent "Data Science," the wwPDB is introducing several new policies: (i) Collection of ORCID (Open Researcher and Contributor ID: <http://orcid.org/>) that is implemented in 2016 and will expand to all entry authors, (ii) Introduction of a versioning system that allows depositors of record to update their own previously released entries. Upon introduction of the file versioning system, the current 4-characters PDB ID will change. These issues will be introduced at the Seminar.

2. Querying the PDBj Mine2 relational database

PDBj Mine2 関係データベースを検索する

Akira R. Kinjo, Institute for Protein Research, Osaka University

PDBj Mine2 RDB is the relational database for PDBj. It can be directly accessed via the interactive web interface at <https://pd bj.org/mine/sql> or via the REST API at https://pd bj.org/rest/mine2_sql (see <https://pd bj.org/help/rest-interface> for the details of the REST API). Furthermore, a complete database dump is available at <ftp://ftp.pd bj.org/mine2/> for local installation using PostgreSQL (<https://www.postgresql.org/>) version 9.3 or higher (see <https://pd bj.org/help/mine2-rdb-local-install> for the instruction). Most of the tables in PDBj Mine2 RDB correspond to the categories defined in the PDBx/mmCIF dictionary (<http://mmcif.wwpdb.org/>). For a complete description of the database schema, see <https://pd bj.org/mine-rdb-docs>. We have also integrated the SIFTS resource (<https://www.ebi.ac.uk/pdbe/docs/sifts/>). Currently, only the "quick access" files of SIFTS are incorporated in the PDBj Mine2 RDB, the table structures of which reflect the tab-separated format of the original SIFTS files (see <https://pd bj.org/help/sifts> for the detail). A comprehensive list of examples are available at <https://pd bj.org/help/mine2-sql>. In this seminar, I will explain the basic structure of the database as well as effective ways to query it.

3. Situation, utilization and visualization of cryo-EM structure data

クライオ電子顕微鏡データの現状、見方、使い方

Hirofumi Suzuki, Institute for Protein Research, Osaka University

Recent innovation in cryo-EM methodology gave significant impact to structural biology and databanks for its data, EMDB and PDB. To utilize such the multiscale hybrid structure data, PDBj provide Web-based services, EM Navigator, Yorodumi, and Omokage search. New version of PDBx/mmCIF format supports better-organized information especially about experimental information of EM. In the seminar, we will introduce news about the structure data, improvement of the tools, and our new collaborative effort with wwPDB members.